



Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.18 [Mar-02-2008]

 Matrix **BLOSUM62** gap open: **11** gap extension: **1**

 x_dropoff: **0** expect: **10.00** wordsize: **3** Filter View option **Standard**

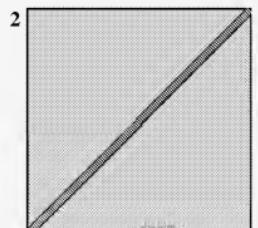
 Masking character option **X for protein, n for nucleot** Masking color option **Black**
 Show CDS translation

Sequence 1: [gi|6706916|spike glycoprotein \[bovine coronavirus\]](#) Genbank Accession# AAF25499

Length = 1363 (1 .. 1363)

Sequence 2: unnamed protein product SEQ ID NO: 4

Length = 1363 (1 .. 1363)



NOTE: Bitscore and expect value are calculated based on the size of the nr database.

Score = 2625 bits (6803), Expect = 0.0
 Identities = 1311/1363 (96%), Positives = 1337/1363 (98%), Gaps = 0/1363 (0%)

| | | |
|-----------|---|-----|
| Query 1 | MFLILLISLPMALAVIGDLKCTTVSINDVTGVPBVSTDVDTNGLGTYYVLDRVYLNT | 60 |
| | MFLILLISLPMA AVIGDLKCTTVSINDVTG PS+STD VDVTNGLGTYYVLDRVYLNT | |
| Sbjct 1 | MFLILLISLPMAFAVIGDLKCTTVSINDVTGAPSISTDVVDVTNGLGTYYVLDRVYLNT | 60 |
| Query 61 | TLLLNGYYPTSGSTYRNMALKGTLKLSTLWFKPPLSDFINGIFAKVKNTKVIKNGVMYS | 120 |
| | TLLLNGYYPTSGSTYRNMALKGTLKLSTLWFKPPLSDFI+G+FAKVKNTRVIK+GV+YS | |
| Sbjct 61 | TLLLNGYYPTSGSTYRNMALKGTLKLSTLWFKPPLSDFIDGVFAKVKNTRVIKDGVVYS | 120 |
| Query 121 | EFPAITIGSTFVNNTSYSVVVQPHHTNLDNKLQGLLEISVCQYTMCYEPHTICHPNLGNRR | 180 |

| | | | |
|-------|-----|--|-----|
| Sbjct | 121 | EFPAITIGSTFVNNTSYSVVVQPHHTNLDNKLQGLLEISVCQYTM+CYPHT+CHPNLGN+R EFPAITIGSTFVNNTSYSVVVQPHHTNLDNKLQGLLEISVCQYTMCDYPHTMCHPNLGNKR | 180 |
| Query | 181 | IELWHDWTGVVSCLYKRNFTYDVNADYLYHFYQEGGTIFYAYFTDTGVVTKFVLNVYLGT IELWHDWTGVV CLYKRNFTYDVNADYLY HFYQEGGTIFYAYFTDTGVVTKFVL+FVLGTT | 240 |
| Sbjct | 181 | IELWHDWTGVVPCLYKRNFTYDVNADYLYSHFYQEGGTIFYAYFTDTGVVTKFHVYLGT | 240 |
| Query | 241 | VLSHYYVMPLTCNSAMTLEYWVTPLTSKQYLLAFNQDGIVIFNAVDCKSDFMSEIKCKTLS VLSHYYVMPLTCNSAMTLEYWVTPLT KQYLLAFNQDGIVIFNAVDCKSDFMSEIKCKTLS | 300 |
| Sbjct | 241 | VLSHYYVMPLTCNSAMTLEYWVTPLTFKQYLLAFNQDGIVIFNAVDCKSDFMSEIKCKTLS | 300 |
| Query | 301 | IAPSTGVYELNGYTVPPIADYVRRIPNLPCNCIEAWLNDKSVPSPLNWERKTFNSNCNFNM IAPSTGVYELNGYTVPPIADYVRRIPNLPCNCIEAWLNDKSVPSPLNWERKTFNSNCNFNM | 360 |
| Sbjct | 301 | IAPSTGVYELNGYTVPPIADYVRRIPNLPCNCIEAWLNDKSVPSPLNWERKTFNSNCNFNM | 360 |
| Query | 361 | SSLMSFIQADSFTCNNIDAAKIYGMCFSSITIDKFAIPNGRKVDLQLGNLGYLQSFnYRI SSLMSFIQADSFTCNNIDAAKIYGMCF SITIDKFAIPNGRKVDLQ+GNLGYLQSFnYRI | 420 |
| Sbjct | 361 | SSLMSFIQADSFTCNNIDAAKIYGMCFSSITIDKFAIPNGRKVDLQMGNLGYLQSFnYRI | 420 |
| Query | 421 | DTTATSCQLYYNLPAAANVSRSFNPSWNRFFTEQSFKPQPVGVFDTDHDVVYQAHCFC DTTATSCQLYYNLPAA+NVS+SRFNPS WNRFFTEQSFKPQPVGVFDTDHDVVYQAHCFC | 480 |
| Sbjct | 421 | DTTATSCQLYYNLPASNVSIISRFNPSIWNRRFFTEQSFKPQPVGVFDTDHDVVYQAHCFC | 480 |
| Query | 481 | KAPTNFCPCKLDGSILCVGSGSIDAGYKNSGIGTCPAGTNYLTCHAAQCNCCLCTPDPIT KAPTNFCPCKL+GSLCVGSG GIDAGYKNSGIGTCPAGTNYLTC+NA QC+CLCTPDPIT | 540 |
| Sbjct | 481 | KAPTNFCPCKLNGLSILCVGSGFIDAGYKNSGIGTCPAGTNYLTCCYNAQCDCCLCTPDPIL | 540 |
| Query | 541 | SKSTGPYKCPQTKYLVGIGEHCSGLAIKSDYCGGNPCTCQPAFLGWSVDSCLQGDRCNI SKSTGPYKCPQTKYLVGIGEHCSGLAIKSDYCGGNPCTCQPAFLGWSVDSCLQGDRCNI | 600 |
| Sbjct | 541 | SKSTGPYKCPQTKYLVGIGEHCSGLAIKSDYCGGNPCTCQPAFLGWSVDSCLQGDRCNI | 600 |
| Query | 601 | FANFILHDVNSGTTCSTDLQKSNTDIILGCVVNYDLYGITGQGIFVEVNATYYNSQNLL FANFILH VNSGTTCSTDLQKSNTDIILGCVVNYDLYGITGQGIFVEVNATYYNSQNLL | 660 |
| Sbjct | 601 | FANFILHGvnSGTTCSTDLQKSNTDIILGCVVNYDLYGITGQGIFVEVNATYYNSQNLL | 660 |
| Query | 661 | YDSNGNLYGFRDYLNTNRTFMIRSCYSGRVSAAFHANSSEPALFRNIKCNYVFNNTLSRQ YDSNGNLYGFRDYLNTNRTFMIRSCYSGRVSA FH+NSSEPALFRNIKCNYVFNNTLSRQ | 720 |
| Sbjct | 661 | YDSNGNLYGFRDYLNTNRTFMIRSCYSGRVSAGFHNSSEPALFRNIKCNYVFNNTLSRQ | 720 |
| Query | 721 | LQPINYFDSYLGCVVNAJDNSTSSAVQTCDLTVGSGYCVDYSTKRRSRAITTGYRFTNFE LQPINYFDSYLGCVVNAJDNSTSS+VQTCDLTVGSGY DYST+RRSRR ITTGYRFTNFE | 780 |
| Sbjct | 721 | LQPINYFDSYLGCVVNAJDNSTSSVQTCDLTVGSGYWDYSTQRSSRRTITTGYRFTNFE | 780 |
| Query | 781 | PFTVNSVNDSELPGGLYEIQIPSEFTIGNMEEFIQISSPKVTIDCSAFVCGDYAACKSQ PFTVNVNDSELPGGLYEIQIPSEFTIGNMEEFIQ SPKVTIDC FVCGDYAACKSQ | 840 |
| Sbjct | 781 | PFTVNPVNDSLHPVGGLYEIQIPSEFTIGNMEEFIQTRSPKVTDPCPVFCGDYAACKSQ | 840 |
| Query | 841 | LVEYGSFCDNINAILTEVNELLDTTQLQVANSLMNGVTLSTKLKGVNFnVDDINFSPLV | 900 |

Blast Result

| | | | |
|-------|------|--|------|
| Sbjct | 841 | LVEYGSFCDNINAILTEVNELLDTTQLQVANSLMNGVTLSTKLKD G NFNVDDINFSPVL LVEYGSFCDNINAILTEVNELLDTTQLQVANSLMNGVTLSTKLKDGFNFNVDINFSPVL | 900 |
| Query | 901 | GCLGSDCNVKSSRSAIEDLLLFSKVKLSDVGVFVEAYNNCTGGAEIRDLCVQS YNGIKVLP GCLGS+CNKVSSRSAIEDLLLFSKVKLSDVGVF+AYNNCTGGAEIRDLCVQS YNGIKVLP | 960 |
| Sbjct | 901 | GCLGSECNVKSSRSAIEDLLLFSKVKLSDVGFDAYNNCTGGAEIRDLCVQS YNGIKVLP | 960 |
| Query | 961 | PLLSENQISGYTLAATSASLFPWSAAAGVPFYLNVQYRINGIGVTM DVL S QNQKLI A NA PLLSENQISGYTLAAT ASLFPPWSAAAGVPFYLNVQYRINGIGVTM DVL +QNQKLI+NA | 1020 |
| Sbjct | 961 | PLLSENQISGYTLAATFASLFPWSAAAGVPFYLNVQYRINGIGVTM DVL T QNQKLI SNA | 1020 |
| Query | 1021 | FNNALDAI QEGFDATNSALVKIQAVVNANA E ALNNLLQQLS NRFGA ISSLQ EILSR LDA FNNALDAI QEGFDATNSALVKIQAVVNANA E ALNNLLQQLS N+FGAIS+SLQ EILSR LDA | 1080 |
| Sbjct | 1021 | FNNALDAI QEGFDATNSALVKIQAVVNANA E ALNNLLQQLS NKFGA ISASLQ EILSR LDA | 1080 |
| Query | 1081 | LEAQAOQIDRLINGRLTALNAYVSQQLSDSTLVKFSAQAMEKVNECVKSQSSRINF CNG LEAQAOQIDRLINGRLTALNAYVSQQLSDSTLVKFSAQAMEKVNECVKSQSSRINF CNG | 1140 |
| Sbjct | 1081 | LEAQAOQIDRLINGRLTALNAYVSQQLSDSTLVKFSAQAMEKVNECVKSQSSRINF CNG | 1140 |
| Query | 1141 | NHIISLVQNAPYGLYFIHF SYVPTKYV TAKVSPGLCIAGDRGIAPKSGYFVN VNNNTWMFT NHIISLVQNAPYGLYFIHF SYVPTKYV TAKVSPGLCIAGDRGIAPKSGYFVN VNNNTWMFT | 1200 |
| Sbjct | 1141 | NHIISLVQNAPYGLYFIHF SYVPTKYV TAKVSPGLCIAGDRGIAPKSGYFVN VNNNTWMFT | 1200 |
| Query | 1201 | GSGYYYPEPITGNV VVV M STCAV NYTKAPDVM LNISTPNLPDFKEELDQWFKNQ TSVAPD GSGYYYPEPITGNV VVV M STCAV NYTKAPDVM LNISTPNLPDFKEELDQWFKNQ T +APD | 1260 |
| Sbjct | 1201 | GSGYYYPEPITGNV VVV M STCAV NYTKAPDVM LNISTPNLPDFKEELDQWFKNQ TL MAPD | 1260 |
| Query | 1261 | LSLDYINVTF L D L QDE MN RL QEA IKV L N QSYI N L K D I G T Y E Y Y V K W P W Y V W L L I G L A G V A LSLDYINVTF L D L QDE MN RL QEA IKV L N QSYI N L K D I G T Y E Y Y V K W P W Y V W L L I G L A G V A | 1320 |
| Sbjct | 1261 | LSLDYINVTF L D L QDE MN RL QEA IKV L N H S YI N L K D I G T Y E Y Y V K W P W Y V W L L I G L A G V A | 1320 |
| Query | 1321 | MLVLLFFFICCCTGCGTSCFKKCGGCCDDYTGHQELVIKTS H D D MLVLLFFFICCCTGCGTSCFKKCGGCCDDYTGHQELVIKTS H D D | 1363 |
| Sbjct | 1321 | MLVLLFFFICCCTGCGTSCFKKCGGCCDDYTGHQELVIKTS H D D | 1363 |

CPU time: 0.05 user secs. 0.03 sys. secs 0.08 total secs.